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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,209A

DATE: 04/26/2001
TIME: 12:14:36

Input Set : A:\190337.txt
Output Set: N:\CRF3\04262001\I530209A.raw

SEQUENCE LISTING
```
   3 (1) GENERAL INFORMATION:
   5       (i) APPLICANT: Inze, Dirk
   6                      De Veylder Lieven
   7                      De Almeida Janice
   9      (ii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof
  11     (iii) NUMBER OF SEQUENCES: 4
C--> 13     (iv) CORRESPONDENCE ADDRESS:
  14            (A) ADDRESSEE: Nixon Peabody LLP
  15            (B) STREET: 990 Stewart Avenue
  16            (C) CITY: Garden City
  17            (D) STATE: New York, New York
C--> 18            (F) ZIP: 11530
  20      (v) COMPUTER READABLE FORM:
  21            (A) MEDIUM TYPE: Floppy disk
  22            (B) COMPUTER: IBM PC compatible
  23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  26     (vi) CURRENT APPLICATION DATA:
C--> 27            (A) APPLICATION NUMBER: US/09/530,209A
C--> 28            (B) FILING DATE: 13-Jun-2000
  29            (C) CLASSIFICATION:
  31    (vii) PRIOR APPLICATION DATA:
  32            (A) APPLICATION NUMBER: EP PCT/EP98/06749
  33            (B) FILING DATE: 23-OCT-1998
  34            (A) APPLICATION NUMBER: EP 97.203.303.9
  35            (B) FILING DATE: 24-OCT-1997
  38 (2) INFORMATION FOR SEQ ID NO: 1:
  40      (i) SEQUENCE CHARACTERISTICS:
  41            (A) LENGTH: 927 base pairs
  42            (B) TYPE: nucleic acid
  43            (C) STRANDEDNESS: double
  44            (D) TOPOLOGY: linear
  46     (ii) MOLECULE TYPE: cDNA
  48    (iii) HYPOTHETICAL: NO
  50     (ix) FEATURE:
  51            (A) NAME/KEY: CDS
  52            (B) LOCATION:1..927
  54     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
  56 ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC        48
  57 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn
  58   1               5                  10                  15
  60 GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG        96
  61 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser
  62              20                  25                  30
  64 ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG       144
  65 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met
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RAW SEQUENCE LISTING   DATE: 04/26/2001
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```
66          35                        40                         45
68 GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC          192
69 Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile
70      50                        55                         60
72 AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT          240
73 Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp
74  65                      70                         75                80
76 GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA          288
77 Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro
78                      85                         90                 95
80 TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT          336
81 Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val
82              100                   105                    110
84 CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG          384
85 His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val
86              115                   120                    125
88 GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG          432
89 Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met
90      130                   135                    140
92 TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA          480
93 Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys
94 145                   150                    155                    160
96 TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA          528
97 Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg
98                      165                   170                    175
100 TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG          576
101 Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys
102              180                   185                    190
104 ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA          624
105 Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser
106          195                   200                    205
108 TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT          672
109 Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe
110     210                   215                    220
112 AGA CCT TCT GAA GCT GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA          720
113 Arg Pro Ser Glu Ala Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
114 225                   230                    235                    240
116 TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA          768
117 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
118                  245                   250                    255
120 CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT          816
121 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
122              260                   265                    270
124 GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA          864
125 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
126              275                   280                    285
128 TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT          912
129 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr
130      290                   295                    300
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```
132 ACA CAT CTT TCT TAA                                          927
133 Thr His Leu Ser
134 305
137 (2) INFORMATION FOR SEQ ID NO: 2:
139       (i) SEQUENCE CHARACTERISTICS:
140             (A) LENGTH: 308 amino acids
141             (B) TYPE: amino acid
142             (D) TOPOLOGY: linear
144       (ii) MOLECULE TYPE: protein
145       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
147 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn
148   1               5                  10                  15
150 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser
151              20                  25                  30
153 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met
154          35                  40                  45
156 Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile
157      50                  55                  60
159 Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp
160  65                  70                  75                  80
162 Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro
163                  85                  90                  95
165 Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val
166              100                 105                 110
168 His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val
169          115                 120                 125
171 Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met
172      130                 135                 140
174 Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys
175 145                 150                 155                 160
177 Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg
178                  165                 170                 175
180 Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys
181              180                 185                 190
183 Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser
184          195                 200                 205
186 Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe
187      210                 215                 220
189 Arg Pro Ser Glu Ala Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
190 225                 230                 235                 240
192 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
193              245                 250                 255
195 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
196              260                 265                 270
198 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
199          275                 280                 285
201 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr
202      290                 295                 300
204 Thr His Leu Ser
```

205 305
208 (2) INFORMATION FOR SEQ ID NO: 3:
210   (i) SEQUENCE CHARACTERISTICS:
211   (A) LENGTH: 25 base pairs
212   (B) TYPE: nucleic acid
213   (C) STRANDEDNESS: single
214   (D) TOPOLOGY: linear
216   (ii) MOLECULE TYPE: other nucleic acid
217   (A) DESCRIPTION: /desc = "oligonucleotide"
219   (iii) HYPOTHETICAL: YES
221   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
223 GAACACTCGA GTGTAATGGC AGAGG   25
227 (2) INFORMATION FOR SEQ ID NO: 4:
229   (i) SEQUENCE CHARACTERISTICS:
230   (A) LENGTH: 26 base pairs
231   (B) TYPE: nucleic acid
232   (C) STRANDEDNESS: single
233   (D) TOPOLOGY: linear
235   (ii) MOLECULE TYPE: other nucleic acid
236   (A) DESCRIPTION: /desc = "oligonucleotide"
238   (iii) HYPOTHETICAL: YES
240   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
242 CATCATACTA GTTATAATAA TGTAAG   26

VERIFICATION SUMMARY   DATE: 04/26/2001
PATENT APPLICATION: **US/09/530,209A**   TIME: 12:14:41

Input Set : **A:\190337.txt**
Output Set: **N:\CRF3\04262001\I530209A.raw**

L:13 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]
L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]